



#11

SEQUENCE LISTING

<110> Barber, Elizabeth K

<120> Gene Expression Control Element DNA

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<140> US/09/966,264C

<141> 2001-09-28

<150> US/60/237,079

<151> 2000-09-30

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<170> PatentIn version 3.1

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tga act cag gtg tgc aca att atc agg aac acc cca aaa cca aag tga 95
Thr Gln Val Cys Thr Ile Ile Arg Asn Thr Pro Lys Pro Lys
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Gly Arg Asn Ser Met Arg Ser Arg Val Cys Leu Ile
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taa gta atc aat caa tca ctc ata gcc aag gtg gaa aag atg tat ccc 96
Val Ile Asn Gln Ser Leu Ile Ala Lys Val Glu Lys Met Tyr Pro
20 25 30

atc atg gaa tat tcc tgt tct gat aga aat ctt gtg ctt atc tat gga 144
Ile Met Glu Tyr Ser Cys Ser Asp Arg Asn Leu Val Leu Ile Tyr Gly
35 40 45

att ctt ttg ata tat att tac att ggg aac ctg aat gta gct tga cat 192
Ile Leu Leu Ile Tyr Ile Gly Asn Leu Asn Val Ala His
50 55 60

ttt tcc atg taa aca cca gta gcc tga tcc aac att aag ctg ata cta 240
Phe Ser Met Thr Pro Val Ala Ser Asn Ile Lys Leu Ile Leu
65 70 75

aca aac aac gtg taa tgg ctt cat taa taa ggc ttt gct tct tcc tgg 288
Thr Asn Asn Val Trp Leu His Gly Phe Ala Ser Ser Trp
80 85

aaa ctg gtg aaa aat caa acc ttg ttg tgt aca ccc tcg atg cag ctt 336
Lys Leu Val Lys Asn Gln Thr Leu Leu Cys Thr Pro Ser Met Gln Leu
90 95 100

ctg tgt tgt ctt cac cca gaa atg ggg aat gat ttc cca aat ggc aaa 384
Leu Cys Cys Leu His Pro Glu Met Gly Asn Asp Phe Pro Asn Gly Lys
105 110 115 120

gaa aca gag tga tgc tat cta tct gca cct ttt gta aag tct gtc ttt 432
Glu Thr Glu Cys Tyr Leu Ser Ala Pro Phe Val Lys Ser Val Phe
125 130 135

ctt tct ctt tgt ttt cca gga cac aat gta gga agt ctt ttc cac atg 480
Leu Ser Leu Cys Phe Pro Gly His Asn Val Gly Ser Leu Phe His Met
140 145 150

gca gat gat ttg ggc aga gcg atg gag tcc tta gta tca gtc atg aca 528
Ala Asp Asp Leu Gly Arg Ala Met Glu Ser Leu Val Ser Val Met Thr
155 160 165

gat gaa gaa gga gca gaa taa atg ttt tac aac tcc tga ttc ccg cat 576
Asp Glu Glu Gly Ala Glu Met Phe Tyr Asn Ser Phe Pro His
170 175 180

ggt ttt tat aat att cat aca aca aag agg att aga cag taa gag ttt 624
Gly Phe Tyr Asn Ile His Thr Thr Lys Arg Ile Arg Gln Glu Phe
185 190 195

aca aga aat aaa tct ata ttt ttg tga agg gta gtg gta tta tac tgt 672
Thr Arg Asn Lys Ser Ile Phe Leu Arg Val Val Val Leu Tyr Cys
200 205 210

aga ttt cag tag ttt cta agt ctg tta ttg ttt tgt taa caa tgg cag 720
Arg Phe Gln Phe Leu Ser Leu Leu Phe Cys Gln Trp Gln
215 220 225

gtt tta cac gtc tat gca att gta caa aaa agt tat aag aaa act aca 768
Val Leu His Val Tyr Ala Ile Val Gln Lys Ser Tyr Lys Lys Thr Thr
230 235 240

tgt aaa atc ttg ata gct aaa taa ctt gcc att tct tta tat gga acg 816
Cys Lys Ile Leu Ile Ala Lys Leu Ala Ile Ser Leu Tyr Gly Thr
245 250 255

cat ttt ggg ttg ttt aaa aat tta taa cag tta taa aga aag aat tat 864
His Phe Gly Leu Phe Lys Asn Leu Gln Leu Arg Lys Asn Tyr
260 265 270

aaa gga aaa aga aaa taa cgc aat gga caa gtg gtg aag ctg tga act 912
Lys Gly Lys Arg Lys Arg Asn Gly Gln Val Val Lys Leu Thr
275 280

cag gtg tgc aca att atc agg aac acc cca aaa cca aag tga ggt aga 960
Gln Val Cys Thr Ile Ile Arg Asn Thr Pro Lys Pro Lys Gly Arg
285 290 295

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Glu Glu

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ccagtagcct gatccaac

18

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caggacacaa tgttagga

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Ile Tyr Ile Tyr Ile Gly Asn Leu Asn Met Lys Lys Glu Gln Asn Lys
35 40 45

Cys Phe Thr Thr Pro Asp Ser Arg Met Val Phe Ile Ile Phe Ile Gln
50 55 60

Gln Arg Gly Leu Asp Ser Lys Ser Leu Gln Glu Ile Asn Leu Tyr Phe
65 70 75 80

Cys Glu Gly Phe Tyr Thr Ser Met Gln Leu Tyr Lys Lys Val Ile Arg
85 90 95

Lys Leu His Lys Ile Thr Gln Trp Thr Arg Thr Pro Gln Asn Gln Ser
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20 25 30

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35 40 45

Gly Asn Leu Asn Val Ala Arg His Phe Ser Met Lys Thr Pro Val Ala
50 55 60

Arg Ser Asn Ile Lys Leu Ile Leu Thr Asn Asn Val Lys Trp Leu His
65 70 75 80

Lys Lys Gly Phe Ala Ser Ser Trp Lys Leu Val Lys Asn Gln Thr Leu
85 90 95

Leu Cys Thr Pro Ser Met Gln Leu Leu Cys Cys Leu His Pro Glu Met
100 105 110

Gly Asn Asp Phe Pro Asn Gly Lys Glu Thr Glu Arg Cys Tyr Leu Ser
115 120 125

Ala Pro Phe Val Lys Ser Val Phe Leu Ser Leu Cys Phe Pro Gly His
130 135 140

Asn Val Gly Ser Leu Phe His Met Ala Asp Asp Leu Gly Arg Ala Met
145 150 155 160

Glu Ser Leu Val Ser Val Met Thr Asp Glu Glu Gly Ala Glu Lys Met
165 170 175

Phe Tyr Asn Ser Arg Phe Pro His Gly Phe Tyr Asn Ile His Thr Thr
180 185 190

Lys Arg Ile Arg Gln Lys Glu Phe Thr Arg Asn Lys Ser Ile Phe Leu
195 200 205

Arg Arg Val Val Val Leu Tyr Cys Arg Phe Gln Lys Phe Leu Ser Leu
210 215 220

Leu Leu Phe Cys Lys Gln Trp Gln Val Leu His Val Tyr Ala Ile Val
225 230 235 240

Gln Lys Ser Tyr Lys Lys Thr Thr Cys Lys Ile Leu Ile Ala Lys Lys
245 250 255

Leu Ala Ile Ser Leu Tyr Gly Thr His Phe Gly Leu Phe Lys Asn Leu
260 265 270

Lys Gln Leu Lys Arg Lys Asn Tyr Lys Gly Lys Arg Lys Lys Arg Asn
275 280 285

Gly Gln Val Val Lys Leu Arg Thr Gln Val Cys Thr Ile Ile Arg Asn
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Cys Lys Leu Ile

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att att att ttc aac cca agt aaa agc aga gag aaa ata gcc acc tcc 96
Ile Ile Ile Phe Asn Pro Ser Lys Ser Arg Glu Lys Ile Ala Thr Ser
20 25 30

acc ata gcc tca gaa gca agc caa cag cct gaa aca gct ttg aaa tga 144
Thr Ile Ala Ser Glu Ala Ser Gln Gln Pro Glu Thr Ala Leu Lys
35 40 45

aaa gtt ggt gtg gcg gtg atg gtg gca gtg ata atg gtg acc gat ggt 192
Lys Val Gly Val Ala Val Met Val Ala Val Ile Met Val Thr Asp Gly
50 55 60

tgg gtg ctg gtg atg gta gtg gta gtt gtg aag gtg gtg atg 234
Trp Val Leu Val Met Val Val Val Val Lys Val Val Met
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Tyr Lys Gly Lys Arg Lys
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Arg Asn Gly Gln Val Val Lys Leu
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Thr Gln Val Cys Thr Ile Ile Arg Asn Thr Pro Lys Pro Lys
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Gly Arg Asn Ser Met Arg Ser Arg Val
1 5

<210> 38
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Leu Ile Val Lys Lys Met Phe Val Asn Thr Ser Arg Glu
1 5 10

<210> 39
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Val Ile Asn Gln Ser Leu Ile Ala Lys Val Glu Lys Met Tyr Pro
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Ile Met Glu Tyr Ser Cys Ser Asp Arg Asn Leu Val Leu Ile Tyr
20 25 30

Gly Ile Leu Leu Ile Tyr Ile Tyr Ile Gly Asn Leu Asn Val Ala
35 40 45

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Ser Asn Ile Lys Leu Ile Leu Thr Asn Asn Val
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Gly Phe Ala Ser Ser Trp Lys Leu Val Lys Asn Gln Thr Leu Leu
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Cys Thr Pro Ser Met Gln Leu Leu Cys Cys Leu His Pro Glu Met
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Gly Asn Asp Phe Pro Asn Gly Lys Glu Thr Glu
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Cys Tyr Leu Ser Ala Pro Phe Val Lys Ser Val Phe Leu Ser Leu
1 5 10 15

Cys Phe Pro Gly His Asn Val Gly Ser Leu Phe His Met Ala Asp
20 25 30

Asp Leu Gly Arg Ala Met Glu Ser Leu Val Ser Val Met Thr Asp
35 40 45

Glu Glu Gly Ala Glu
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Glu Phe Thr Arg Asn Lys Ser Ile Phe Leu
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Arg Val Val Val Leu Tyr Cys Arg Phe Gln
1 5 10

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Phe Leu Ser Leu Leu Leu Phe Cys
1 5

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Gln Trp Gln Val Leu His Val Tyr Ala Ile Val Gln Lys Ser Tyr
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Lys Lys Thr Thr Cys Lys Ile Leu Ile Ala Lys
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Leu Ala Ile Ser Leu Tyr Gly Thr His Phe Gly Leu Phe Lys Asn Leu
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Arg Lys Asn Tyr Lys Gly Lys Arg Lys
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Phe Ile Ile Ile Ile Phe Asn Pro Ser Lys Ser Arg Glu Lys Ile Ala
-60 -55 -50

acc tcc acc ata gcc tca gaa gca agc caa cag cct gaa aca gct ttg 141
Thr Ser Thr Ile Ala Ser Glu Ala Ser Gln Gln Pro Glu Thr Ala Leu
-45 -40 -35

aaa tga aaa gtt ggt gtg gcg gtg atg gtg gca gtg ata atg gtg acc 189
Lys Lys Val Gly Val Ala Val Met Val Ala Val Ile Met Val Thr
-30 -25 -20

gat ggt tgg gtg ctg gtg atg gta gtg gtt gtg aag gtg gtg atg 237
Trp Val Leu Val Met Val Val Val Val Lys Val Val Met Asp Gly
-15 -10 -5

gtg gtt tga ttg ata gta aaa aaa atg ttc gtt aat aca agt aga gag 285
Val Val Leu Ile Val Lys Lys Met Phe Val Asn Thr Ser Arg Glu
1 5 10 15

taa gta atc aat caa tca ctc ata gcc aag gtg gaa aag atg tat ccc 333
Val Ile Asn Gln Ser Leu Ile Ala Lys Val Glu Lys Met Tyr Pro
20 25 30

atc atg gaa tat tcc tgg tct gat aga aat ctt gtg ctt atc tat gga 381
Ile Met Glu Tyr Ser Cys Ser Asp Arg Asn Leu Val Leu Ile Tyr Gly

35

40

45

att ctt ttg ata tat att tac att ggg aac ctg aat gta gct tga cat 429
 Ile Leu Leu Ile Tyr Ile Tyr Ile Gly Asn Leu Asn Val Ala His
 50 55 60

ttt tcc atg taa aca cca gta gcc tga tcc aac att aag ctg ata cta 477
 Phe Ser Met Thr Pro Val Ala Ser Asn Ile Lys Leu Ile Leu
 65 70 75

aca aac aac gtg taa tgg ctt cat taa taa ggc ttt gct tct tcc tgg 525
 Thr Asn Asn Val Trp Leu His Gly Phe Ala Ser Ser Trp
 80 85

aaa ctg gtg aaa aat caa acc ttg ttg tgt aca ccc tcg atg cag ctt 573
 Lys Leu Val Lys Asn Gln Thr Leu Leu Cys Thr Pro Ser Met Gln Leu
 90 95 100

ctg tgt tgt ctt cac cca gaa atg ggg aat gat ttc cca aat ggc aaa 621
 Leu Cys Cys Leu His Pro Glu Met Gly Asn Asp Phe Pro Asn Gly Lys
 105 110 115 120

gaa aca gag tga tgc tat cta tct gca cct ttt gta aag tct gtc ttt 669
 Glu Thr Glu Cys Tyr Leu Ser Ala Pro Phe Val Lys Ser Val Phe
 125 130 135

ctt tct ctt tgt ttt cca gga cac aat gta gga agt ctt ttc cac atg 717
 Leu Ser Leu Cys Phe Pro Gly His Asn Val Gly Ser Leu Phe His Met
 140 145 150

gca gat gat ttg ggc aga gcg atg gag tcc tta gta tca gtc atg aca 765
 Ala Asp Asp Leu Gly Arg Ala Met Glu Ser Leu Val Ser Val Met Thr
 155 160 165

gat gaa gaa gca gaa taa atg ttt tac aac tcc tga ttc ccg cat 813
 Asp Glu Glu Gly Ala Glu Met Phe Tyr Asn Ser Phe Pro His
 170 175 180

ggt ttt tat aat att cat aca aca aag agg att aga cag taa gag ttt 861
 Gly Phe Tyr Asn Ile His Thr Thr Lys Arg Ile Arg Gln Glu Phe
 185 190 195

aca aga aat aaa tct ata ttt ttg tga agg gta gtg gta tta tac tgt 909
 Thr Arg Asn Lys Ser Ile Phe Leu Arg Val Val Val Leu Tyr Cys
 200 205 210

aga ttt cag tag ttt cta agt ctg tta ttg ttt tgt taa caa tgg cag 957
 Arg Phe Gln Phe Leu Ser Leu Leu Phe Cys Gln Trp Gln
 215 220 225

gtt tta cac gtc tat gca att gta caa aaa agt tat aag aaa act aca 1005
 Val Leu His Val Tyr Ala Ile Val Gln Lys Ser Tyr Lys Lys Thr Thr
 230 235 240

tgt aaa atc ttg ata gct aaa taa ctt gcc att tct tta tat gga acg 1053
 Cys Lys Ile Leu Ile Ala Lys Leu Ala Ile Ser Leu Tyr Gly Thr
 245 250 255

cat ttt ggg ttg ttt aaa aat tta taa cag tta taa aga aag aat tat 1101
His Phe Gly Leu Phe Lys Asn Leu Gln Leu Arg Lys Asn Tyr
260 265 270

aaa gga aaa aga aaa taa cgc aat gga caa gtg gtg aag ctg tga act 1149
Lys Gly Lys Arg Lys Arg Asn Gly Gln Val Val Lys Leu Thr
275 280

cag gtg tgc aca att atc agg aac acc cca aaa cca aag tga ggt aga 1197
Gln Val Cys Thr Ile Ile Arg Asn Thr Pro Lys Pro Lys Gly Arg
285 290 295

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300 305

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<211> 47

<212> PRT

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<400> 52

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35 40 45

Leu Lys

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<213> human

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20 25 30

Val Val

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<211> 1044

<212> DNA

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ccaacaaagt gtgaaaggtg tgtgccattha cacatcttc tcggtgataa 200
gagcccttgc tatgaagttc tgagatgtgt taggaagatg aatcatcaat 250
ttacatttct ccccatcaaa tgacaccatg ctgatccagt attaagctaa 300
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tgtcttttcc tgaaaatggta atgactccca atagtgccaa ccaggggtac 450
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agtccttagt ttcaagtcatg acagatgaag aaggaggcaga ataaatgttt 600
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tatggAACGC attttgggtt gttaaaaat ttataacagt tataaagaaa 900
gattgtaaac taaagtgtgc tttataaaaaa aagtgttttca aaaaaacccc 950
taaacaaaca cacacgcaca cacacacaca cacacacaca cacacacaca 1000
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agttggtgatgg gcggtgatgg tggcagtat aatggtgacc gatggttggg 200
tgctggtgat ggttagtggta gttgtgaagg tggtgatggt ggtttgattt 250
atagtaaaaa aaatgttcgt taatacaagt agagagtaag taatcaatca 300
atcactcata gccaaaggatgg aaaagatgta tcccatcatg gaatattcct 350
gttctgatag aaatcttgcgt cttatctatg gaattctttt gatatatattt 400
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Asn Val Ala Arg His Phe Ser Met Lys Thr Pro Val Ala Arg Ser
35 40 45

Asn Ile Lys Leu Ile Leu Thr Asn Asn Val Lys Trp Leu His Lys
50 55 60

Lys Gly Phe Ala Ser Ser Trp Lys Leu Val Lys Asn Gln Thr Leu
65 70 75

Leu Cys Thr Pro Ser Met Gln Leu Leu Cys Cys Leu His Pro Glu
80 85 90

Met Gly Asn Asp Phe Pro Asn Gly Lys Glu Thr Glu Arg Cys Tyr
95 100 105

Leu Ser Ala Pro Phe Val Lys Ser Val Phe Leu Ser Leu Cys Phe
110 115 120

Pro Gly His Asn Val Gly Ser Leu Phe His Met Ala Asp Asp Leu
125 130 135

Gly Arg Ala Met Glu Ser Leu Val Ser Val Met Thr Asp Glu Glu
140 145 150

Gly Ala Glu Lys Met Phe Tyr Asn Ser Arg Phe Pro His Gly Phe
155 160 165

Tyr Asn Ile His Thr Thr Lys Arg Ile Arg Gln Lys Glu Phe Thr
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Arg Asn Lys Ser Ile Phe Leu Arg Arg Val Val Val Leu Tyr Cys
185 190 195

Arg Phe Gln Lys Phe Leu Ser Leu Leu Phe Cys Lys Gln Trp
200 205 210

Gln Val Leu His Val Tyr Ala Ile Val Gln Lys Ser Tyr Lys Lys
215 220 225

Thr Thr Cys Lys Ile Leu Ile Ala Lys Lys Leu Ala Ile Ser Leu
230 235 240

Tyr Gly Thr His Phe Gly Leu Phe Lys Asn Leu Lys Gln Leu Lys
245 250 255

Arg Lys Asn Tyr Lys Gly Lys Arg Lys Lys Arg Asn Gly Gln Val
260 265 270

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Lys Leu Ile

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Met Tyr Pro Ile Met Glu Tyr Ser Cys Ser Asp Arg Asn Leu Val
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Leu Ile Tyr Gly Ile Leu Leu Ile Tyr Ile Tyr Ile Gly Asn Leu
20 25 30

Asn Met Lys Lys Glu Gln Asn Lys Cys Phe Thr Thr Pro Asp Ser
35 40 45

Arg Met Val Phe Ile Ile Phe Ile Gln Gln Arg Gly Leu Asp Ser
50 55 60

Lys Ser Leu Gln Glu Ile Asn Leu Tyr Phe Cys Glu Gly Phe Tyr
65 70 75

Thr Ser Met Gln Leu Tyr Lys Lys Val Ile Arg Lys Leu His Lys
80 85 90

Ile Thr Gln Trp Thr Arg Thr Pro Gln Asn Gln Ser Glu Val Glu

95 100 105

Ile Ala